

SEQUENCE LISTING

<110> Advanced Technologies (Cambridge) Ltd

<120> Plant Limit Dextrinase Inhibitor

<130> RD-ATC-32

<140>

<141>

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 517

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (14) .. (457)

<400> 1

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1 5 10	
gcc gtc ttg ctc tcg gtc ctc gcc gtc gcc gcc gcc acc ctg gag agc	97
Ala Val Leu Leu Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser	
15 20 25	
gtc aag gac gag tgc caa cca ggg gtg gac ttc ccg cat aac ccg tta	145
Val Lys Asp Glu Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu	
30 35 40	
gcc acc tgc cac acc tac gtg ata aaa cgg gtc tgc ggc cgc ggt ccc	193
Ala Thr Cys His Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro	
45 50 55 60	
agc cgg ccc atg ctg gtg aag gag cgg tgc tgc cgg gag ctg gcg gcc	241
Ser Arg Pro Met Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala	
65 70 75	
gtc ccg gat cac tgc cgg tgc gag gcg ctg cgc atc ctc atg gac ggg	289
Val Pro Asp His Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly	
80 85 90	
gtg cgc acg ccg gag ggc cgc gtg gtt gag gga cgg ctc ggt gac agg	337
Val Arg Thr Pro Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg	
95 100 105	
cgt gac tgc ccg agg gag gag cag agg gcg ttc gcc gcc acg ctt gtc	385
Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val	
110 115 120	
acg gcg gcg gag tgc aac cta tcg tcc gtc cag gag ccg gga gta cgc	433
Thr Ala Ala Glu Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg	
125 130 135 140	

ttg gtg cta ctg gca gat gga tga cgatcgaaat gcgccaaggt aatgaagcgg 487.
 Leu Val Leu Leu Ala Asp Gly
 145

agtactgtat acagaataaa agtactcgag 517

<210> 2

<211> 147

<212> PRT

<213> Hordeum vulgare

<400> 2

Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly Ala Val Leu Leu
 1 5 10 15
 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu
 20 25 30
 Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His
 35 40 45
 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met
 50 55 60
 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala Val Pro Asp His
 65 70 75 80
 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro
 85 90 95
 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro
 100 105 110
 Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val Thr Ala Ala Glu
 115 120 125
 Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg Leu Val Leu Leu
 130 135 140
 Ala Asp Gly
 145

<210> 3

<211> 672

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (39)..(482)

<400> 3

aagagattga accaacgacc aataaaactag tatcaaca atg gca tcc gac cat cgt 56
 Met Ala Ser Asp His Arg
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 cgc ttc gtc ctc tcc ggc gcc gtc ttg ctc tcg gtc ctc gcc gtc gcc 104
 Arg Phe Val Leu Ser Gly Ala Val Leu Leu Ser Val Leu Ala Val Ala
 10 15 20
 gcc gcc acc ttg gag agc gtc aag gac gag tgc caa cta ggg gtg gac 152
 Ala Ala Thr Leu Glu Ser Val Lys Asp Glu Cys Gln Leu Gly Val Asp
 25 30 35
 ttc ccg cat aac ccg tta gcc acc tgc cac acc tac gtg ata aaa cgg 200
 Phe Pro His Asn Pro Leu Ala Thr Cys His Thr Tyr Val Ile Lys Arg
 40 45 50

gtc tgc ggc cgc ggt ccc agc cgg ccc atg ctg gtg aag gag cgg tgc 248
 Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu Val Lys Glu Arg Cys
 55 60 65 70

tgc cgg gag ctg gcg gcc gtc ccg gat cac tgc cgg tgc gag gcg ctg 296
 Cys Arg Glu Leu Ala Val Pro Asp His Cys Arg Cys Glu Ala Leu
 75 80 85

cgc atc ctc atg gac ggg gtg cgc acg ccg gag ggc cgc gtg gtt gag 344
 Arg Ile Leu Met Asp Gly Val Arg Thr Pro Glu Gly Arg Val Val Glu
 90 95 100

gga cgg ctc ggt gac agg cgt gac tgc ccg agg gag gag cag agg gcg 392
 Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala
 105 110 115

ttc gcc gcc acg ctt gtc acg gcg gcg gag tgc aac cta tcg tcc gtc 440
 Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys Asn Leu Ser Ser Val
 120 125 130

cag gcg ccg gga gta cgc ttg gtg cta ctg gca gat gga tga 482
 Gln Ala Pro Gly Val Arg Leu Val Leu Leu Ala Asp Gly
 135 140 145

cgatgcaaat gcgccaaggt aatgaagcgg agtactgtat acagaataaaa agtactcgag 542

tgaaaacaaa ctcataaata aaccttgtga gatgtatgcg tatgatctat ggtgtggaca 602

gttaaattgt ggccgattga tgaataaaaa aggttgaac aaattaaatt gttgtggggtt 662

catatactat 672

<210> 4

<211> 147

<212> PRT

<213> Hordeum vulgare

<400> 4

Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly Ala Val Leu Leu
 1 5 10 15
 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu
 20 25 30
 Cys Gln Leu Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His
 35 40 45
 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met
 50 55 60
 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala Val Pro Asp His
 65 70 75 80
 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro
 85 90 95
 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro
 100 105 110
 Arg Glu Glu Gln Arg Ala Phe Ala Thr Leu Val Thr Ala Ala Glu
 115 120 125
 Cys Asn Leu Ser Ser Val Gln Ala Pro Gly Val Arg Leu Val Leu Leu
 130 135 140
 Ala Asp Gly
 145

<210> 6
 <211> 153
 <212> PRT
 <213> Triticum aestivum

<400> 6
 Met Ala Ser Asn His Arg Arg Phe Leu Leu Ser Gly Ala Val Leu Leu
 1 5 10 15
 Ser Val Leu Ala Ala Val Ala Ala Leu Glu Ser Val Glu Asp Glu Cys
 20 25 30
 Gln Pro Gly Val Ala Phe Pro His Asn Ala Leu Ala Thr Cys His Thr
 35 40 45
 Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu
 50 55 60
 Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Val Val Pro Asp Tyr Cys
 65 70 75 80
 Arg Cys Glu Ala Leu Arg Val Leu Met Asp Gly Val Arg Ala Glu Glu
 85 90 95
 Gly His Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg
 100 105 110
 Glu Ala Gln Arg Glu Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys
 115 120 125
 Asn Leu Pro Thr Val Ser Gly Val Gly Ser Thr Leu Gly Ala Thr Gly
 130 135 140
 Arg Trp Met Thr Ile Glu Leu Pro Lys
 145 150

<210> 7
 <211> 444
 <212> DNA

<213> Hordeum spontaneum

<220>
 <221> CDS
 <222> (1)..(444)

<400> 7
 atg gcg ttc aag tac cag ctc ctc ctc tcg gcc gcc gtc atg ctc gcc 48
 Met Ala Phe Lys Tyr Gln Leu Leu Leu Ser Ala Ala Val Met Leu Ala
 1 5 10 15
 att ctc gcc gcc act gtc acc agt ttc ggg gat atg tgt gct cca ggg 96
 Ile Leu Ala Ala Thr Val Thr Ser Phe Gly Asp Met Cys Ala Pro Gly
 20 25 30
 gat gcg ttg cca gcc aac cct ctc aga gcc tgc cgc acc tat gtg gtt 144
 Asp Ala Leu Pro Ala Asn Pro Leu Arg Ala Cys Arg Thr Tyr Val Val
 35 40 45
 agt caa atc tgc cat gta ggc cct aga cta tcc acc tgg gac atg aag 192
 Ser Gln Ile Cys His Val Gly Pro Arg Leu Ser Thr Trp Asp Met Lys
 50 55 60
 agg cgg tgc tgc gac gag ctg tcg gcc atc ccg gcg tac tgc aga tgc 240
 Arg Arg Cys Cys Asp Glu Leu Ser Ala Ile Pro Ala Tyr Cys Arg Cys
 65 70 75 80

```

gag gcg ctg cgt atc atc atg gat ggg aca gta act tgg cag ggt gtg 288
Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val
      85                      90                      95

ttc ggt gcc tac ttc aag gac atg ccc aac tgc cct agg gtg atg caa 336
Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln
      100                      105                      110

acg agc tac gcc gcc aac ctc gtc aac ccg cag gag tgc aac cta tgg 384
Thr Ser Tyr Ala Ala Asn Leu Val Asn Pro Gln Glu Cys Asn Leu Trp
      115                      120                      125

act atc cac ggc agc ccg tcc tgc ccc gaa ctg cag ccc gga tat gaa 432
Thr Ile His Gly Ser Pro Ser Cys Pro Glu Leu Gln Pro Gly Tyr Glu
      130                      135                      140

gtg gtc ttg taa
Val Val Leu
145

```

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<210> 8
<211> 147
<212> PRT
<213> Hordeum spontaneum

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<400> 8
Met Ala Phe Lys Tyr Gln Leu Leu Leu Ser Ala Ala Val Met Leu Ala
  1          5          10          15
Ile Leu Ala Ala Thr Val Thr Ser Phe Gly Asp Met Cys Ala Pro Gly
      20          25          30
Asp Ala Leu Pro Ala Asn Pro Leu Arg Ala Cys Arg Thr Tyr Val Val
      35          40          45
Ser Gln Ile Cys His Val Gly Pro Arg Leu Ser Thr Trp Asp Met Lys
      50          55          60
Arg Arg Cys Cys Asp Glu Leu Ser Ala Ile Pro Ala Tyr Cys Arg Cys
      65          70          75          80
Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val
      85          90          95
Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln
      100          105          110
Thr Ser Tyr Ala Ala Asn Leu Val Asn Pro Gln Glu Cys Asn Leu Trp
      115          120          125
Thr Ile His Gly Ser Pro Ser Cys Pro Glu Leu Gln Pro Gly Tyr Glu
      130          135          140
Val Val Leu
145

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<210> 9
<211> 483
<212> DNA
<213> Oryza sativa

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<220>
<221> CDS
<222> (1)..(483)

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<400> 9

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atg gct tcc aac aag gta gtg ttc tca gtg ttg ctt ctc gcc gtc gtc 48
Met Ala Ser Asn Lys Val Val Phe Ser Val Leu Leu Leu Ala Val Val
1 5 10 15

tcc gtg ctc gcg gcg acg gcg acc atg gcg gag tac cac cac caa gac 96
Ser Val Leu Ala Ala Thr Ala Thr Met Ala Glu Tyr His His Gln Asp
20 25 30

cag gtg gtc tac acc ccg ggc ccg ctc tgt cag cca gga atg ggc tac 144
Gln Val Val Tyr Thr Pro Gly Pro Leu Cys Gln Pro Gly Met Gly Tyr
35 40 45

ccg atg tac ccg ctc ccg cgt tgc cgg gcg ttg gtg aag cgc cag tgc 192
Pro Met Tyr Pro Leu Pro Arg Cys Arg Ala Leu Val Lys Arg Gln Cys
50 55 60

gtc ggc cgt ggc acg gcc gcc gcc gcc gag cag gtc cgg cga gac tgc 240
Val Gly Arg Gly Thr Ala Ala Ala Ala Glu Gln Val Arg Arg Asp Cys
65 70 75 80

tgc cgg cag ctc gcc gcc gtc gac gac agc tgg tgc agg tgc gag gcg 288
Cys Arg Gln Leu Ala Ala Val Asp Asp Ser Trp Cys Arg Cys Glu Ala
85 90 95

atc agc cac atg ctg gga ggc atc tac agg gag ctc ggc gcc ccc gat 336
Ile Ser His Met Leu Gly Gly Ile Tyr Arg Glu Leu Gly Ala Pro Asp
100 105 110

gtc ggg cac ccc atg tcc gag gtg ttc cgc ggc tgc cgg aga ggg gac 384
Val Gly His Pro Met Ser Glu Val Phe Arg Gly Cys Arg Arg Gly Asp
115 120 125

ttg gag cgc gcg gcg gcg agc ctc ccg gcg ttc tgc aac gtg gac atc 432
Leu Glu Arg Ala Ala Ala Ser Leu Pro Ala Phe Cys Asn Val Asp Ile
130 135 140

ccc aac ggc gga ggt ggt gtc tgc tac tgg ctg gcg aga tct ggc tac 480
Pro Asn Gly Gly Gly Gly Val Cys Tyr Trp Leu Ala Arg Ser Gly Tyr
145 150 155 160

tag 483

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<210> 10

<211> 160

<212> PRT

<213> *Oryza sativa*

<400> 10

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Met Ala Ser Asn Lys Val Val Phe Ser Val Leu Leu Leu Ala Val Val
1 5 10 15
Ser Val Leu Ala Ala Thr Ala Thr Met Ala Glu Tyr His His Gln Asp
20 25 30
Gln Val Val Tyr Thr Pro Gly Pro Leu Cys Gln Pro Gly Met Gly Tyr
35 40 45
Pro Met Tyr Pro Leu Pro Arg Cys Arg Ala Leu Val Lys Arg Gln Cys
50 55 60
Val Gly Arg Gly Thr Ala Ala Ala Ala Glu Gln Val Arg Arg Asp Cys
65 70 75 80
Cys Arg Gln Leu Ala Ala Val Asp Asp Ser Trp Cys Arg Cys Glu Ala

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				85					90					95			
Ile	Ser	His	Met	Leu	Gly	Gly	Ile	Tyr	Arg	Glu	Leu	Gly	Ala	Pro	Asp		
			100					105					110				
Val	Gly	His	Pro	Met	Ser	Glu	Val	Phe	Arg	Gly	Cys	Arg	Arg	Gly	Asp		
		115					120					125					
Leu	Glu	Arg	Ala	Ala	Ala	Ser	Leu	Pro	Ala	Phe	Cys	Asn	Val	Asp	Ile		
	130					135					140						
Pro	Asn	Gly	Gly	Gly	Gly	Val	Cys	Tyr	Trp	Leu	Ala	Arg	Ser	Gly	Tyr		
145					150					155					160		

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<210> 11
<211> 707
<212> DNA
<213> Triticum durum
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<220>  
<221> CDS  
<222> (27) .. (533)
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<400> 11																	
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Met Ala Cys Lys Ser Ser Cys Ser Leu																	
1 5																	
ctc	ctc	ttg	gcc	gcc	gtc	ctg	ctc	tcc	gtc	ttg	gcc	gct	gct	tcc	gcc	101	
Leu	Leu	Leu	Ala	Ala	Val	Leu	Leu	Ser	Val	Leu	Ala	Ala	Ala	Ser	Ala		
10					15					20					25		
tcc	ggc	agc	tgc	gtc	cca	ggg	gtg	gct	ttt	cgg	acc	aat	ctt	ctg	cca	149	
Ser	Gly	Ser	Cys	Val	Pro	Gly	Val	Ala	Phe	Arg	Thr	Asn	Leu	Leu	Pro		
				30					35					40			
cac	tgc	cgc	gac	tat	gtg	tta	caa	caa	act	tgt	ggc	acc	ttc	acc	cct	197	
His	Cys	Arg	Asp	Tyr	Val	Leu	Gln	Gln	Thr	Cys	Gly	Thr	Phe	Thr	Pro		
			45					50					55				
ggg	tca	aag	tta	ccc	gaa	tgg	atg	aca	tct	gcg	tcg	ata	tac	tcc	cct	245	
Gly	Ser	Lys	Leu	Pro	Glu	Trp	Met	Thr	Ser	Ala	Ser	Ile	Tyr	Ser	Pro		
		60					65					70					
ggg	aaa	ccg	tac	ctc	gcc	aag	ttg	tat	tgc	tgc	cag	gag	ctc	gca	gaa	293	
Gly	Lys	Pro	Tyr	Leu	Ala	Lys	Leu	Tyr	Cys	Cys	Gln	Glu	Leu	Ala	Glu		
	75					80					85						
att	tct	cag	cag	tgc	cgg	tgc	gag	gcg	ctg	cgc	tac	ttc	ata	gcg	ttg	341	
Ile	Ser	Gln	Gln	Cys	Arg	Cys	Glu	Ala	Leu	Arg	Tyr	Phe	Ile	Ala	Leu		
90					95					100					105		
ccg	gta	ccg	tct	cag	cct	gtg	gac	ccg	agg	tcc	ggc	aat	gtt	ggt	gag	389	
Pro	Val	Pro	Ser	Gln	Pro	Val	Asp	Pro	Arg	Ser	Gly	Asn	Val	Gly	Glu		
				110					115					120			
agc	ggc	ctc	atc	gat	ctg	ccc	gga	tgc	ccc	agg	gag	atg	caa	tgg	gac	437	
Ser	Gly	Leu	Ile	Asp	Leu	Pro	Gly	Cys	Pro	Arg	Glu	Met	Gln	Trp	Asp		
			125					130					135				
ttc	gtc	aga	tta	ctc	gtc	gcc	ccg	ggg	cag	tgc	aac	ttg	gcg	acc	att	485	
Phe	Val	Arg	Leu	Leu	Val	Ala	Pro	Gly	Gln	Cys	Asn	Leu	Ala	Thr	Ile		
		140					145					150					

cac aat gtt cga tac tgc ccc gcc gtg gaa cag cct ctg tgg atc tag 533
 His Asn Val Arg Tyr Cys Pro Ala Val Glu Gln Pro Leu Trp Ile
 155 160 165

agataaaatc agtcgctcgt gaataagcat gcatgttgca tccataggcg tgtgggtgtgc 593
 atgtatacat atgtgagctc cgcgcgctca acatgtgtgg gctatctgct atgaatgaga 653
 ataaagagaa tcattctgtg gttctttaat ttcaactaaa aaaaaaaaaa aaaa 707

<210> 12
 <211> 168
 <212> PRT
 <213> Triticum durum

<400> 12
 Met Ala Cys Lys Ser Ser Cys Ser Leu Leu Leu Leu Ala Ala Val Leu
 1 5 10 15
 Leu Ser Val Leu Ala Ala Ala Ser Ala Ser Gly Ser Cys Val Pro Gly
 20 25 30
 Val Ala Phe Arg Thr Asn Leu Leu Pro His Cys Arg Asp Tyr Val Leu
 35 40 45
 Gln Gln Thr Cys Gly Thr Phe Thr Pro Gly Ser Lys Leu Pro Glu Trp
 50 55 60
 Met Thr Ser Ala Ser Ile Tyr Ser Pro Gly Lys Pro Tyr Leu Ala Lys
 65 70 75 80
 Leu Tyr Cys Cys Gln Glu Leu Ala Glu Ile Ser Gln Gln Cys Arg Cys
 85 90 95
 Glu Ala Leu Arg Tyr Phe Ile Ala Leu Pro Val Pro Ser Gln Pro Val
 100 105 110
 Asp Pro Arg Ser Gly Asn Val Gly Glu Ser Gly Leu Ile Asp Leu Pro
 115 120 125
 Gly Cys Pro Arg Glu Met Gln Trp Asp Phe Val Arg Leu Leu Val Ala
 130 135 140
 Pro Gly Gln Cys Asn Leu Ala Thr Ile His Asn Val Arg Tyr Cys Pro
 145 150 155 160
 Ala Val Glu Gln Pro Leu Trp Ile
 165

<210> 13
 <211> 712
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (33)..(500)

<400> 13
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 Met Ala Ser Ser Ser Ser Ser
 1 5
 agc cac cgc cgc ctc atc ctc gca gcc gcc gtc ctg ctc tcc gtg ctc 101
 Ser His Arg Arg Leu Ile Leu Ala Ala Val Leu Leu Ser Val Leu
 10 15 20

gcg gct gcc agc gcc agc gcc ggg acc tcc tgc gtg ccg ggg tgg gcc 149
 Ala Ala Ala Ser Ala Ser Ala Gly Thr Ser Cys Val Pro Gly Trp Ala
 25 30 35

atc ccg cac aac ccg ctc ccg agc tgc cgc tgg tac gtg acc agc cgg 197
 Ile Pro His Asn Pro Leu Pro Ser Cys Arg Trp Tyr Val Thr Ser Arg
 40 45 50 55

acc tgc ggc atc ggg ccg cgc ctc ccg tgg ccg gag ctg aag agg aga 245
 Thr Cys Gly Ile Gly Pro Arg Leu Pro Trp Pro Glu Leu Lys Arg Arg
 60 65 70

tgc tgc ccg gag ctg gcg gac atc ccg gcg tac tgc ccg tgc acg gcg 293
 Cys Cys Arg Glu Leu Ala Asp Ile Pro Ala Tyr Cys Arg Cys Thr Ala
 75 80 85

ctg agc atc ctc atg gac ggc gcg atc ccg cct ggc ccg gac gcg cag 341
 Leu Ser Ile Leu Met Asp Gly Ala Ile Pro Pro Gly Pro Asp Ala Gln
 90 95 100

ctg gag ggc cgc cta gag gac ctg ccg ggc tgc ccg ccg gag gtg cag 389
 Leu Glu Gly Arg Leu Glu Asp Leu Pro Gly Cys Pro Arg Glu Val Gln
 105 110 115

agg gga ttc gcc gcc acc ctc gtc acg gag gcc gag tgc aac ctg gcc 437
 Arg Gly Phe Ala Ala Thr Leu Val Thr Glu Ala Glu Cys Asn Leu Ala
 120 125 130 135

acc atc agc ggc gtc gcc gaa tgc ccc tgg att ctc ggc ggc gga acg 485
 Thr Ile Ser Gly Val Ala Glu Cys Pro Trp Ile Leu Gly Gly Gly Thr
 140 145 150

atg ccc tcc aag taa ctgcgaagag catagtgcac gaggaatgag cttgtagcta 540
 Met Pro Ser Lys
 155

gctcatatgt ctgaataata agcacagcaa gaagatgaat gcatttctcg gatcgttcat 600

ccggaacaat aattaaagg gatccggatt tgttcttgtg atataattaa cgattcctgt 660

tataacttga agtagctagg ctgcgtcccca tccaatgcaa gcaaaaaaaaa aa 712

<210> 14
 <211> 155
 <212> PRT
 <213> Zea mays

<400> 14
 Met Ala Ser Ser Ser Ser Ser Ser His Arg Arg Leu Ile Leu Ala Ala
 1 5 10 15
 Ala Val Leu Leu Ser Val Leu Ala Ala Ser Ala Ser Ala Gly Thr
 20 25 30
 Ser Cys Val Pro Gly Trp Ala Ile Pro His Asn Pro Leu Pro Ser Cys
 35 40 45
 Arg Trp Tyr Val Thr Ser Arg Thr Cys Gly Ile Gly Pro Arg Leu Pro
 50 55 60
 Trp Pro Glu Leu Lys Arg Arg Cys Cys Arg Glu Leu Ala Asp Ile Pro
 65 70 75 80

Ala	Tyr	Cys	Arg	Cys	Thr	Ala	Leu	Ser	Ile	Leu	Met	Asp	Gly	Ala	Ile
				85					90					95	
Pro	Pro	Gly	Pro	Asp	Ala	Gln	Leu	Glu	Gly	Arg	Leu	Glu	Asp	Leu	Pro
			100					105					110		
Gly	Cys	Pro	Arg	Glu	Val	Gln	Arg	Gly	Phe	Ala	Ala	Thr	Leu	Val	Thr
		115				120						125			
Glu	Ala	Glu	Cys	Asn	Leu	Ala	Thr	Ile	Ser	Gly	Val	Ala	Glu	Cys	Pro
		130				135						140			
Trp	Ile	Leu	Gly	Gly	Gly	Thr	Met	Pro	Ser	Lys					
145					150					155					

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<210> 15
<211> 122
<212> PRT
<213> Eleusine coracana
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```

<400> 15
Ser Val Gly Thr Ser Cys Ile Pro Gly Met Ala Ile Pro His Asn Pro
  1          5          10          15
Leu Asp Ser Cys Arg Trp Tyr Val Ala Lys Arg Ala Cys Gly Val Gly
          20          25          30
Pro Arg Leu Ala Thr Gln Glu Met Lys Ala Arg Cys Cys Arg Gln Leu
          35          40          45
Glu Ala Ile Pro Ala Tyr Cys Arg Cys Glu Ala Val Arg Ile Leu Met
          50          55          60
Asp Gly Val Val Thr Pro Ser Gly Gln His Glu Gly Arg Leu Leu Gln
          65          70          75          80
Asp Leu Pro Gly Cys Pro Arg Gln Val Gln Arg Ala Phe Ala Pro Lys
          85          90          95
Leu Val Thr Glu Val Glu Cys Asn Leu Ala Thr Ile His Gly Gly Pro
          100          105          110
Phe Cys Leu Ser Leu Leu Gly Ala Gly Glu
          115          120

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<210> 16
<211> 121
<212> PRT
<213> Secale cereale
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```

<400> 16
Ser Val Gly Gly Gln Cys Val Pro Gly Leu Ala Met Pro His Asn Pro
  1                               10                      15

Leu Gly Ala Cys Arg Thr Tyr Val Val Ser Gln Ile Cys His Val Gly
  20          25          30

Pro Arg Leu Phe Thr Trp Asp Met Lys Arg Arg Cys Cys Asp Glu Leu
  35          40          45

Leu Ala Ile Pro Ala Tyr Cys Arg Cys Glu Ala Leu Arg Ile Leu Met
  50          55          60

```

Asp Gly Val Val Thr Gln Gln Gly Val Phe Glu Gly Gly Tyr Leu Lys
65 70 75 80

Asp Met Pro Asn Cys Pro Arg Val Thr Gln Arg Ser Tyr Ala Ala Thr
85 90 95

Leu Val Ala Pro Gln Glu Cys Asn Leu Pro Thr Ile His Gly Ser Pro
100 105 110

Tyr Cys Pro Thr Leu Gln Ala Gly Tyr
115 120

<210> 17

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 17

accaataaac tagtatcaac aatggcatcc gacca

35

<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 18

ccaacctttt ttattcatca atcgccaca

30

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 19

tcggattcca ttgccagct atctgtc

27

<210> 20

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 20

atgggccta acaatcagta aattgaacg

29

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 21
cgggtaccggc aggctgaagt cca

23

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 22
ccggggatct accatgagcc caga

24

<210> 23
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 23
gaatgaaccg aaaccggcgg ta

22

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 24
taccacctcc ctgagggttg

20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

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20